

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KARIN, MICHAEL
HIBI, MASAHIKO
LIN, ANNING

(ii) TITLE OF INVENTION: ONCOPROTEIN PROTEIN KINASE

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: FISH & RICHARDSON P.C.
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(C) CITY: La Jolla
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/444,393
(B) FILING DATE: 19-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Haile, Ph.D., Lisa A.,
(B) REGISTRATION NUMBER: 38,347
(C) REFERENCE/DOCKET NUMBER: 07257/017002

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 678-5070
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
(B) CLONE: c-Jun/JNK binding site

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..47

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser
1 5 10 15

Leu Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro
20 25 30

Asp Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:
(B) CLONE: N-terminal primer

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTGCAGGAT CCCCATGACT GCAAAGATGG AAACG

35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

64

(B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTGCAGGAT CCCCGACGAT GCCCTAACG CCTC

34

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCTGCAGGAT CCCCGAGAGC GGACCTTATG GCTAC

35

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCTGCAGGAT CCCCGCCGAC CCAGTGGGGA GCCTG

35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: N-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTGCAGGAT CCCCAAGAAC TCGGACCTCC TCACC

35

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGAATTCTGC AGGCGCTCCA GCTCGGGCGA

30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: C-terminal primer

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGAATTCCCTG CAGGTGGCG CG TGGTGGTGAT GTG

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Jun

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 414..1406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCCGGG GCGGCCAAGA CCCGCCGCCG GCCGGCCACT GCAGGGTCCG CACTGATCCG	60
CTCCGGCGGA GAGCCGCTGC TCTGGGAAGT GAGTCGCCT GCGGACTCCG AGGAACCGCT	120
GCGCACGAAG AGCGCTCAGT GAGTGACCGC GACTTTCAA AGCCGGGTAG CGCGCGCGAG	180
TCGACAAGTA AGAGTGCAGG AGGCATCTTA ATTAACCTG CGCTCCCTGG AGCGAGCTGG	240
TGAGGAGGGC GCAGCGGGGA CGACAGCCAG CGGGTGCCTG CGCTCTTACA GAAACTTCC	300

CTGTCAAAGG CTCCGGGGGG CGCGGGTGTG CCCCCGTTGC CAGAGCCCTG TTGCGGCC	360		
GAAACTTGTG CGCGCACGCC AAACTAACCT CACGTGAAGT GACGGACTGT TCT ATG	416		
Met			
1			
ACT GCA AAG ATG GAA ACG ACC TTC TAT GAC GAT GCC CTC AAC GCC TCG	464		
Thr Ala Lys Met Glu Thr Thr Phe Tyr Asp Asp Ala Leu Asn Ala Ser			
5	10	15	
TTC CTC CCG TCC GAG AGC GGA CCT TAT GGC TAC AGT AAC CCC AAG ATC	512		
Phe Leu Pro Ser Glu Ser Gly Pro Tyr Gly Tyr Ser Asn Pro Lys Ile			
20	25	30	
CTG AAA CAG AGC ATG ACC CTG AAC CTG GCC GAC CCA GTG GGG AGC CTG	560		
Leu Lys Gln Ser Met Thr Leu Asn Leu Ala Asp Pro Val Gly Ser Leu			
35	40	45	
AAG CCG CAC CTC CGC GCC AAG AAC TCG GAC CTC CTC ACC TCG CCC GAC	608		
Lys Pro His Leu Arg Ala Lys Asn Ser Asp Leu Leu Thr Ser Pro Asp			
50	55	60	65
GTG GGG CTG CTC AAG CTG GCG TCG CCC GAG CTG GAG CGC CTG ATA ATC	656		
Val Gly Leu Leu Lys Leu Ala Ser Pro Glu Leu Glu Arg Leu Ile Ile			
70	75	80	
CAG TCC AGC AAC GGG CAC ATC ACC ACC ACG CCG ACC CCC ACC CAG TTC	704		
Gln Ser Ser Asn Gly His Ile Thr Thr Thr Pro Thr Pro Thr Gln Phe			
85	90	95	
CTG TGC CCC AAG AAC GTG ACA GAT GAG CAG GAG GGG TTC GCC GAG GGC	752		
Leu Cys Pro Lys Asn Val Thr Asp Glu Gln Glu Gly Phe Ala Glu Gly			
100	105	110	
TTC GTG CGC GCC CTG GCC GAA CTG CAC AGC CAG AAC ACG CTG CCC AGC	800		
Phe Val Arg Ala Leu Ala Glu Leu His Ser Gln Asn Thr Leu Pro Ser			
115	120	125	
GTC ACG TCG GCG GCG CAG CCG GTC AAC GGG GCA GGC ATG GTG GCT CCC	848		
Val Thr Ser Ala Ala Gln Pro Val Asn Gly Ala Gly Met Val Ala Pro			
130	135	140	145
GCG GTA GCC TCG GTG GCA GGG GGC AGC GGC AGC GGC GGC TTC AGC GCC	896		
Ala Val Ala Ser Val Ala Gly Gly Ser Gly Ser Gly Gly Phe Ser Ala			
150	155	160	
AGC CTG CAC AGC GAG CCG CCG GTC TAC GCA AAC CTC AGC AAC TTC AAC	944		
Ser Leu His Ser Glu Pro Pro Val Tyr Ala Asn Leu Ser Asn Phe Asn			
165	170	175	
CCA GGC GCG CTG AGC AGC GGC GGC GGG GCG CCC TCC TAC GGC GCG GCC	992		
Pro Gly Ala Leu Ser Ser Gly Gly Ala Pro Ser Tyr Gly Ala Ala			
180	185	190	

GGC CTG GCC TTT CCC GCG CAA CCC CAG CAG CAG CAG CCG CCG CAC Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Pro Pro His 195 200 205	1040
CAC CTG CCC CAG CAG ATG CCC GTG CAG CAC CCG CGG CTG CAG GCC CTG His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala Leu 210 215 220 225	1088
AAG GAG GAG CCT CAG ACA GTG CCC GAG ATG CCC GGC GAG ACA CCG CCC Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro Pro 230 235 240	1136
CTG TCC CCC ATC GAC ATG GAG TCC CAG GAG CGG ATC AAG GCG GAG AGG Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu Arg 245 250 255	1184
AAG CGC ATG AGG AAC CGC ATC GCT GCC TCC AAG TGC CGA AAA AGG AAG Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg Lys 260 265 270	1232
CTG GAG AGA ATC GCC CGG CTG GAG GAA AAA GTG AAA ACC TTG AAA GCT Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala 275 280 285	1280
CAG AAC TCG GAG CTG GCG TCC ACG GCC AAC ATG CTC AGG GAA CAG GTG Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val 290 295 300 305	1328
GCA CAG CTT AAA CAG AAA GTC ATG AAC CAC GTT AAC AGT GGG TGC CAA Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys Gln 310 315 320	1376
CTC ATG CTA ACG CAG CAG TTG CAA ACA TTT TGAAGAGAGA CCGTCGGGG Leu Met Leu Thr Gln Gln Leu Gln Thr Phe 325 330	1426
CTGAGGGCA ACGAAGAAAA AAAATAACAC AGAGAGACAG ACTTGAGAAC TTGACAAGTT	1486
GCGACGGAGA GAAAAAAGAA GTGTCCGAGA ACTAAAGCCA AGGGTATCCA AGTTGGACTG	1546
GGTTCGGTCT GACGGCGCCC CCAGTGTGCA CGAGTGGAA GGACTTGGTC GCGCCCTCCC	1606
TTGGCGTGGG GCCAGGGAGC GGCGCCTGC GGGCTGCCCG GCTTGCAGA CGGGCTGTCC	1666
CCGCGCGAAC GGAACGTTGG ACTTTCGTTA ACATTGACCA AGAACTGCAT GGACCTAACAA	1726
TTCGATCTCA TTCAGTATTA AAGGGGGGAG GGGGAGGGGG TTACAAACTG CAATAGAGAC	1786
TGTAGATTGC TTCTGTAGTA CTCCCTTAAGA ACACAAAGCG GGGGGAGGGT TGGGGAGGGG	1846
CGGCAGGAGG GAGGTTGTG AGAGCGAGGC TGAGCCTACA GATGAACCTCT TTCTGGCCTG	1906
CTTCGTTAA CTGTGTATGT ACATATATAT ATTTTTAAT TTGATTAAAG CTGATTACTG	1966

TCAATAAAC	GCTTCATGCC	TTTGTAAAGTT	ATTTCTTGT	TGTTTGTTTG	GGTATCCTGC	2026	
CCAGTGTTGT	TTGTAAATAA	GAGATTTGGA	GCAC	CTGAG	TTTACCA	TTT	2086
ATATAATT	TTT						2099

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Thr	Ala	Lys	Met	Glu	Thr	Thr	Phe	Tyr	Asp	Asp	Ala	Leu	Asn	Ala
1				5				10					15		
Ser	Phe	Leu	Pro	Ser	Glu	Ser	Gly	Pro	Tyr	Gly	Tyr	Ser	Asn	Pro	Lys
				20				25					30		
Ile	Leu	Lys	Gln	Ser	Met	Thr	Leu	Asn	Leu	Ala	Asp	Pro	Val	Gly	Ser
				35				40					45		
Leu	Lys	Pro	His	Leu	Arg	Ala	Lys	Asn	Ser	Asp	Leu	Leu	Thr	Ser	Pro
				50				55					60		
Asp	Val	Gly	Leu	Leu	Lys	Leu	Ala	Ser	Pro	Glu	Leu	Glu	Arg	Leu	Ile
				65				70					80		
Ile	Gln	Ser	Ser	Asn	Gly	His	Ile	Thr	Thr	Thr	Pro	Thr	Pro	Thr	Gln
				85				90					95		
Phe	Leu	Cys	Pro	Lys	Asn	Val	Thr	Asp	Glu	Gln	Glu	Gly	Phe	Ala	Glu
				100				105					110		
Gly	Phe	Val	Arg	Ala	Leu	Ala	Glu	Leu	His	Ser	Gln	Asn	Thr	Leu	Pro
				115				120					125		
Ser	Val	Thr	Ser	Ala	Ala	Gln	Pro	Val	Asn	Gly	Ala	Gly	Met	Val	Ala
				130				135					140		
Pro	Ala	Val	Ala	Ser	Val	Ala	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Phe	Ser
				145				150					155		160
Ala	Ser	Leu	His	Ser	Glu	Pro	Pro	Val	Tyr	Ala	Asn	Leu	Ser	Asn	Phe
				165				170					175		
Asn	Pro	Gly	Ala	Leu	Ser	Ser	Gly	Gly	Ala	Pro	Ser	Tyr	Gly	Ala	
				180				185					190		

Ala Gly Leu Ala Phe Pro Ala Gln Pro Gln Gln Gln Gln Pro Pro
195 200 205

His His Leu Pro Gln Gln Met Pro Val Gln His Pro Arg Leu Gln Ala
210 215 220

Leu Lys Glu Glu Pro Gln Thr Val Pro Glu Met Pro Gly Glu Thr Pro
225 230 235 240

Pro Leu Ser Pro Ile Asp Met Glu Ser Gln Glu Arg Ile Lys Ala Glu
245 250 255

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg
260 265 270

Lys Leu Glu Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
275 280 285

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
290 295 300

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Asn Ser Gly Cys
305 310 315 320

Gln Leu Met Leu Thr Gln Gln Leu Gln Thr Phe
325 330

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